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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=3; day=20; hr=16; min=3; sec=28; ms=753; ]

=====

\*\*\*\*\*

Reviewer Comments:

<150> US 60/430,654

<151> 2002 04 02

Please insert the current Application and date as <140>, and <141>, delete the non-ascii character in date line <151>.

<210> 1

<211> 34

<212> PRT

<213> T. CRUZI

<400> Sequence: 51

The above attached sequence appears after the sequence id 50, If it is a continuation please number is as 51 and change the Total number of sequences in <160> as 57.

\*\*\*\*\*

Application No: 10726692 Version No: 3.0

**Input Set:****Output Set:**

**Started:** 2008-02-29 21:19:36.478  
**Finished:** 2008-02-29 21:19:46.462  
**Elapsed:** 0 hr(s) 0 min(s) 9 sec(s) 984 ms  
**Total Warnings:** 57  
**Total Errors:** 257  
**No. of SeqIDs Defined:** 50  
**Actual SeqID Count:** 57

Error code	Error Description
E 287	Invalid WIPO ST.2 date format; Use (YYYY-MM-DD) in <151>
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)

**Input Set:**

**Output Set:**

**Started:** 2008-02-29 21:19:36.478  
**Finished:** 2008-02-29 21:19:46.462  
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**No. of SeqIDs Defined:** 50  
**Actual SeqID Count:** 57

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed
E 323	Invalid/missing amino acid numbering SEQID (33) POS (995)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1010)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1025)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1040)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1055)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1070)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1085)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1100)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1115)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1130)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1145)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1160)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1175)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1190)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1205)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1220)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1235)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1250)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1265)
E 323	Invalid/missing amino acid numbering SEQID (33) POS (1280) This error has occurred more than 20 times, will not be displayed

Input Set:

Output Set :

**Started:** 2008-02-29 21:19:36.478

**Finished:** 2008-02-29 21:19:46.462

**Elapsed:** 0 hr(s) 0 min(s) 9 sec(s) 984 ms

Total Warnings: 57

Total Errors: 257

No. of SeqIDs Defined: 50

Actual SeqID Count: 57

Error code	Error Description
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna
E 336	Empty lines found between the proteins and the dna This error has occurred more than 20 times, will not be displayed
E 212	Invalid Sequence ID Number; Expected 51 as next SeqID but skipped
E 202	Invalid input format; Value must be an integer in <400> SEQID: (1)

**Input Set:**

**Output Set:**

**Started:** 2008-02-29 21:19:36.478  
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**Total Warnings:** 57  
**Total Errors:** 257  
**No. of SeqIDs Defined:** 50  
**Actual SeqID Count:** 57

Error code	Error Description
E 202	Invalid input format; Value must be an integer in <400> SEQID: (2)
E 249	Order Sequence Error <210> -> <212>; Expected Mandatory Tag: <211> in SEQID ( 3 )
E 202	Invalid input format; Value must be an integer in <400> SEQID: (3)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (4)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (5)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (6)
E 202	Invalid input format; Value must be an integer in <400> SEQID: (7)
E 252	Calc# of Seq. differs from actual; 50 seqIds defined; count=57
E 250	Structural Validation Error; Sequence listing may not be indexable

## SEQUENCE LISTING

<110> KIRCHHOFF, LOUIS V  
KEIKO, OTSU

<120> RECOMBINANT POLYPEPTIDES FOR DIAGNOSING INFECTION WITH  
TRYPANOSOMA CRUZI

<130> PNL21311A

<150> US 60/430,654

<151> 2002 04 02

<160> 50

<170> PatentIn version 3.2

<210> 1

<211> 1521

<212> DNA

<213> T. CRUZI

<220>

<221> CDS

<222> (1)..(1521)

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Tyr Gly Pro Ser Cys Gly Ala Gly Trp Ser Ala Leu Arg Gly Gly	
1 5 10 15	

caa tgc caa caa cct cgt tcg aga aat ctc caa tgg cgt tgt cac ttc	96
Gln Cys Gln Gln Pro Arg Ser Arg Asn Leu Gln Trp Arg Cys His Phe	
20 25 30	

gtt tat tac gga agg act gct ggg ccc atc gta cat caa acc gta cag	144
Val Tyr Tyr Gly Arg Thr Ala Gly Pro Ile Val His Gln Thr Val Gln	
35 40 45	

ccg tac aaa tgg cgc tca tga ctt gtt tgt gtc gga cac ggg caa atc	192
Pro Tyr Lys Trp Arg Ser Leu Val Cys Val Gly His Gly Gln Ile	
50 55 60	

acg cat cat ttt tgc ccc acc tca gaa aaa aac gtt cat cac agt gtt	240
Thr His His Phe Cys Pro Thr Ser Glu Lys Asn Val His His Ser Val	
65 70 75	

tat aac agg att cca gcc gga tgt tct tca aat tag cga gaa gag tcg	288
Tyr Asn Arg Ile Pro Ala Gly Cys Ser Ser Asn Arg Glu Glu Ser	
80 85 90	

ttt gat gtt tgc cat ctg caa ttc cac gaa aat tct tgc gat taa tat	336
Phe Asp Val Cys His Leu Gln Phe His Glu Asn Ser Cys Asp Tyr	
95 100 105	

gca ggg agc cac aac ccc gaa gga gta ctg gca agt tgg aaa tgc gga	384
Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys Gly	
110 115 120	
ctg cat ggg cta tca gag ttc cct cat gct cac gac cga gga gga taa	432
Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly	
125 130 135	
act cct cta cta cgg cat att aaa tgg aac ccc atc cat cat gtc ttt	480
Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe	
140 145 150 155	
acc cgc cac caa aac gaa gac gga agc acc cag aat ttg ccc gga tgt	528
Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys	
160 165 170	
gtt gtt gca gtg gcc aca tgg gcc cat tgt ttc gct tgt gaa tat taa	576
Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr	
175 180 185	
caa aca tgc att tta cgt tgt tac cgc ctc caa tgt ata cat tgt aca	624
Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr	
190 195 200	
tga tgg ctc gta tca tcc gac tgg atc cat ggc cca gct cca aca ggc	672
Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly	
205 210 215	
aga aaa taa tat cac taa ttc caa aaa aga aat gac aaa gct acg aga	720
Arg Lys Tyr His Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg	
220 225 230	
aaa agt gaa aaa ggc cga gaa aga aaa att gga cgc cat taa ccg ggc	768
Lys Ser Glu Lys Gly Arg Glu Arg Lys Ile Gly Arg His Pro Gly	
235 240 245	
aac caa gct gga aga gga acg aaa cca agc gta caa agc agc aca caa	816
Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser Thr Gln	
250 255 260	
ggc aga gga gga aaa ggc taa aac att tca acg cct tat aac att tga	864
Gly Arg Gly Gly Lys Gly Asn Ile Ser Thr Pro Tyr Asn Ile	
265 270 275	
gtc gga aaa tat taa ctt aaa gaa aag gcc aaa tga cgc agt ttc aaa	912
Val Gly Lys Tyr Leu Lys Glu Lys Ala Lys Arg Ser Phe Lys	
280 285 290	
tcg gga taa gaa aaa aaa ttc tga aac cgc aaa aac tga cga agt aga	960
Ser Gly Glu Lys Lys Phe Asn Arg Lys Asn Arg Ser Arg	
295 300	
gaa aca gag ggc ggc tga ggc tgc caa ggc cgt gga gac gga gaa gca	1008
Glu Thr Glu Gly Gly Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala	
305 310 315	

gag ggc agc tga ggc cac gaa ggt tgc cga agc gga gaa gcg gaa ggc	1056
Glu Gly Ser Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly	
320 325 330	
agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga	1104
Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser	
335 340 345	
agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga ggc cgc	1152
Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser Gly Arg	
350 355 360	
caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac gaa ggt	1200
Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His Glu Gly	
365 370 375	
tgc cga agc gga gaa gca gag ggc agc tga agc cat gaa ggt tgc cga	1248
Cys Arg Ser Gly Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg	
380 385 390	
agc gga gaa gca gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga	1296
Ser Gly Glu Ala Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly	
395 400 405	
gaa gca gag ggc agc tga agc cac gaa ggt tgc cga agc gga gaa gca	1344
Glu Ala Glu Gly Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala	
410 415 420	
gaa ggc agc tga ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc	1392
Glu Gly Ser Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly	
425 430 435	
agc tga agc cac gaa ggt tgc cga agc gga gaa gca gaa ggc agc tga	1440
Ser Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser	
440 445 450	
ggc cgc caa ggc cgt gga gac gga gaa gca gag ggc agc tga agc cac	1488
Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser Ser His	
455 460 465	
gaa ggt tgc cga agc gga gaa gga tat cga tcc	1521
Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser	
470 475	

<210> 2  
 <211> 7  
 <212> PRT  
 <213> T. CRUZI

<400> 2

Tyr Gly Pro Ser Cys Gly Ala  
 1 5



<210> 3  
<211> 46  
<212> PRT  
<213> T. CRUZI

<400> 3

Gly Trp Ser Ala Leu Arg Gly Gly Gln Cys Gln Gln Pro Arg Ser Arg  
1 5 10 15

Asn Leu Gln Trp Arg Cys His Phe Val Tyr Tyr Gly Arg Thr Ala Gly  
20 25 30

Pro Ile Val His Gln Thr Val Gln Pro Tyr Lys Trp Arg Ser  
35 40 45

<210> 4  
<211> 36  
<212> PRT  
<213> T. CRUZI

<400> 4

Leu Val Cys Val Gly His Gly Gln Ile Thr His His Phe Cys Pro Thr  
1 5 10 15

Ser Glu Lys Asn Val His His Ser Val Tyr Asn Arg Ile Pro Ala Gly  
20 25 30

Cys Ser Ser Asn  
35

<210> 5  
<211> 18  
<212> PRT  
<213> T. CRUZI

<400> 5

Arg Glu Glu Ser Phe Asp Val Cys His Leu Gln Phe His Glu Asn Ser  
1 5 10 15

Cys Asp

<210> 6  
<211> 32  
<212> PRT

<213> T. CRUZI

<400> 6

Tyr Ala Gly Ser His Asn Pro Glu Gly Val Leu Ala Ser Trp Lys Cys  
1 5 10 15

Gly Leu His Gly Leu Ser Glu Phe Pro His Ala His Asp Arg Gly Gly  
20 25 30

<210> 7

<211> 47

<212> PRT

<213> T. CRUZI

<400> 7

Thr Pro Leu Leu Arg His Ile Lys Trp Asn Pro Ile His His Val Phe  
1 5 10 15

Thr Arg His Gln Asn Glu Asp Gly Ser Thr Gln Asn Leu Pro Gly Cys  
20 25 30

Val Val Ala Val Ala Thr Trp Ala His Cys Phe Ala Cys Glu Tyr  
35 40 45

<210> 8

<211> 16

<212> PRT

<213> T. CRUZI

<400> 8

Gln Thr Cys Ile Leu Arg Cys Tyr Arg Leu Gln Cys Ile His Cys Thr  
1 5 10 15

<210> 9

<211> 17

<212> PRT

<213> T. CRUZI

<400> 9

Trp Leu Val Ser Ser Asp Trp Ile His Gly Pro Ala Pro Thr Gly Arg  
1 5 10 15

Lys

<210> 10  
<211> 23  
<212> PRT  
<213> T. CRUZI

<400> 10

Phe Gln Lys Arg Asn Asp Lys Ala Thr Arg Lys Ser Glu Lys Gly Arg  
1 5 10 15

Glu Arg Lys Ile Gly Arg His  
20

<210> 11  
<211> 24  
<212> PRT  
<213> T. CRUZI

<400> 11

Pro Gly Asn Gln Ala Gly Arg Gly Thr Lys Pro Ser Val Gln Ser Ser  
1 5 10 15

Thr Gln Gly Arg Gly Gly Lys Gly  
20

<210> 12  
<211> 8  
<212> PRT  
<213> T. CRUZI

<400> 12

Asn Ile Ser Thr Pro Tyr Asn Ile  
1 5

<210> 13  
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<212> PRT  
<213> T. CRUZI

<400> 13

Val Gly Lys Tyr  
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<210> 14  
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<213> T. CRUZI

<400> 14

Leu Lys Glu Lys Ala Lys

1 5

<210> 15

<211> 6

<212> PRT

<213> T. CRUZI

<400> 15

Arg Ser Phe Lys Ser Gly

1 5

<210> 16

<211> 4

<212> PRT

<213> T. CRUZI

<400> 16

Glu Lys Lys Phe

1

<210> 17

<211> 4

<212> PRT

<213> T. CRUZI

<400> 17

Asn Arg Lys Asn

1

<210> 18

<211> 8

<212> PRT

<213> T. CRUZI

<400> 18

Arg Ser Arg Glu Thr Glu Gly Gly

1 5

<210> 19

<211> 13

<212> PRT

<213> T. CRUZI

<400> 19

Gly Cys Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 20

<211> 13

<212> PRT

<213> T. CRUZI

<400> 20

Gly His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 21

<211> 13

<212> PRT

<213> T. CRUZI

<400> 21

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 22

<211> 13

<212> PRT

<213> T. CRUZI

<400> 22

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 23

<211> 13

<212> PRT

<213> T. CRUZI

<400> 23

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 24

<211> 13

<212> PRT

<213> T. CRUZI

<400> 24

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 25

<211> 13

<212> PRT

<213> T. CRUZI

<400> 25

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 26

<211> 13

<212> PRT

<213> T. CRUZI

<400> 26

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 27

<211> 13

<212> PRT

<213> T. CRUZI

<400> 27

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 28

<211> 13

<212> PRT

<213> T. CRUZI

<400> 28

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 29

<211> 13

<212> PRT

<213> T. CRUZI

<400> 29

Ser His Glu Gly Cys Arg Ser Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 30

<211> 13

<212> PRT

<213> T. CRUZI

<400> 30

Gly Arg Gln Gly Arg Gly Asp Gly Glu Ala Glu Gly Ser  
1 5 10

<210> 31

<211> 13

<212> PRT

<213> T. CRUZI

<400> 31

Ser His Glu Gly Cys Arg Ser Gly Glu Gly Tyr Arg Ser  
1 5 10

<210> 32

<211> 42

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<213> T CRUZI

<220>

<221> misc\_feature

<222> (1)..(4)

<223> n is a, c, g, or t

<400> 32

nnnnotatta ttgataacagt ttctgtacta tattgggtgt gc

42

<210> 33

<211> 3749

<212> DNA

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<220>

<221> CDS

<222> (833)..(2575)

<220>

<221> sig\_peptide

<222> (833)..(937)

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<220>
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<400> 33
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cgggtcaaaag gatgtatatata tacatatata accataaggg aaacatttgg gcattttaat      120

gcctttacat ttcccttttc cttcaatata ttgtttgttt gtttttgggt tctataggaa      180

attttaggat ccggccagcg gcataggaga ttattctctt ttttattaat tgcttaatgc      240

gttggtctgt gtgtgtgttg gttcccttgt gcgagctcac ggggcctaata tatgattgtt      300

gcgcatatgc atatatatat atatatatat acatgtgtgt gtgtgtgtat atgtacgttt      360

gttggtttgc cgctgtactc ccgcctgcgt gtgtctgtct ctctctctgt gtgtgtgatg      420

ggctgcttct ctttcttttg ttgcgtccct ttattattat tatttttttt tcttctctcc      480

cacttctctc cccgtgtggt gcacgcacag taaagataga gggagaaata gagcgagtgt      540

ttgtatcagt gtctccgttg cggctggtac tggtagaagg agaagaatag aagaaggaga      600

aaaaaaaaaa aaaaaaaaaa aaaagagaga gagagagaga agggcgaacg agaaaaaaga      660

agaagaaaca tttgagaagg aattggaacg aaaattgtaa gaggaagcaa aaaaaaaaaa      720

aaaaagtgtg tgtgtgtgag agagagagag agaggaagcc aataataata aaaagcaaac      780

aaaaaagcaa aaacaaaaat atttgtagac cggacgtccc gtcttggacg tg atg ttt      838
                                     Met Phe
                                     35

tca aaa agg acg tcg cca gca ccc ttc cgt gcg ctc ctg ctg ccg gtc      886
Ser Lys Arg Thr Ser Pro Ala Pro Phe Arg Ala Leu Leu Leu Pro Val
          30                      25                      20

gtg gtg gtg gtg gtg gtg gtg gtg gca tet gtg gcc ctc cct gca gga      934
Val Val Val Val Val Val Val Val Val Ala Ser Val Ala Leu Pro Ala Gly
          15                      10                      5

gcg cag ttt gat tta agg cag cag cag ctg gtt ata cag gat ttc ttc      982
Ala Gln Phe Asp Leu Arg Gln Gln Gln Leu Val Ile Gln Asp Phe Phe
  1  1                      5                      10                      15

atc agt cgc tcc tgc gca gga tgt tca cag ggg caa acc gat ggc cca      1030
Ile Ser Arg Ser Cys Ala Gly Cys Ser Gln Gly Gln Thr Asp Gly Pro
          20                      25                      30

agc ggt gcc ggc aca ctc ttc act gcc gcc ggt ggt tcg ctt ggc aaa      1078
Ser Gly Ala Gly Thr Leu Phe Thr Ala Ala Gly Gly Ser Leu Gly Lys
          35                      40                      45

gat get tcc acg ctg ctg ttg tgt gac caa ggt ggt ggt ggc tcc agc      1126

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Asp Ala Ser Thr Leu Leu Leu Cys Asp Gln Gly Gly Gly Gly Ser Ser	
50 55 60	
gtg cgt ttg gtg aac aaa tcc ggc att ttc acc ctt gcc ggt agt aaa	1174
Val Arg Leu Val Asn Lys Ser Gly Ile Phe Thr Leu Ala Gly Ser Lys	
65 70 75	
acg acg cgt ggc aat caa aat ggt ccg gcg gcg acg gca ctc ttc aac	1222
Thr Thr Arg Gly Asn Gln Asn Gly Pro Ala Ala Thr Ala Leu Phe Asn	
80 85 90 95	
atg ccc cga gct gtg gtg ctt gag gat gga gcg ctt tac gtg gcg gac	1270
Met Pro Arg Ala Val Val Leu Glu Asp Gly Ala Leu Tyr Val Ala Asp	
100 105 110	
agt gcc aac aac ctc gtt cga gaa atc tcc aat ggc att gtc act tcg	1318
Ser Ala Asn Asn Leu Val Arg Glu Ile Ser Asn Gly Ile Val Thr Ser	
115 120 125	
ttt att acg gag gga ctg ctg ggc cca tcg tac atc aaa ccg tac agc	1366
Phe Ile Thr Glu Gly Leu Leu Gly Pro Ser Tyr Ile Lys Pro Tyr Ser	
130 135 140	
cgt cca aat ggc gcc cat gac ttg ttt gtg tcg gac acg ggc aaa tct	1414
Arg Pro Asn Gly Ala His Asp Leu Phe Val Ser Asp Thr Gly Lys Ser	
145 150 155	
cgc atc att ttt gcc cca ctt cag aaa caa acg ttc atc aca gtg ttt	1462
Arg Ile Ile Phe Ala Pro Leu Gln Lys Gln Thr Phe Ile Thr Val Phe	
160 165 170 175	
ata aca gga ttc cag ccg gat gtt ctt caa att agc gag aag agt cgt	1510
Ile Thr Gly Phe Gln Pro Asp Val Leu Gln Ile Ser Glu Lys Ser Arg	
180 185	